



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/733,691
Source: 01PE (1FWO)
Date Processed by STIC: 12/30/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/233,691
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics _____ Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <u>✓</u> _____ Misaligned Amino _____ Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <u>✓</u> _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 _____ "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ.ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> _____ Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 _____ "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



1FWO

RAW SEQUENCE LISTING

DATE: 12/30/2003

PATENT APPLICATION: US/10/733,691

TIME: 11:25:40

Input Set : A:\10733691.txt

Output Set: N:\CRF4\12302003\J733691.raw

pp 1-4

2 <110> APPLICANT: NIKOLICH, MIKELJON
 3 HOOVER, DAVID
 5 <120> TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS INCLUDING ROUGH PHENOTYPE BRUCELLA
 HOST STRAINS
 6 AND COMPLEMENTATION DNA FRAGMENTS
 8 <130> FILE REFERENCE: ARMY 176
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/733,691
 12 <141> CURRENT FILING DATE: 2003-12-11
 14 <150> PRIOR APPLICATION NUMBER: US 60/402,164
 W--> 15 US 60/533,016
 17 <151> PRIOR FILING DATE: 2002-12-12
 W--> 18 2003-09-15
 20 <160> NUMBER OF SEQ ID NOS: 2

list these
together

ERRORED SEQUENCES

E--> 23 <210> SEQ ID NO: SEQ ID NO: 1
 24 <211> LENGTH: LENGTH: 2693
 E--> 25 <212> TYPE: TYPE: DNA
 26 <213> ORGANISM: ORGANISM: Brucella melitensis
 W--> 27 <220> FEATURE: FEATURE:
 E--> 28 <400> SEQUENCE: SEQUENCE: 1

29	caccttatgt	ttgggacatt	ttaattagga	acgtttatgc	40
30	cttcggatgc	cgtgggcgtg	gcatccgcat	gagggatggc	80
31	tttgcgtttc	tgcgctttga	agatggtgaa	attgggtag	120
32	ggccgcaata	tgggtggtga	agcctaccag	catatgagtt	160
33	tcgaaatttt	gaggggttat	ttcttcgccg	caccgaagcc	200
34	actggattgg	atggatatac	agaccttga	tacgtcccag	240
35	atgctgaaca	gcgggggttc	atctttgcag	acggagcagc	280
36	cctccacatc	aatagcctgt	ttgcagataa	taacaagggt	320
37	gatggcgtgt	tttgccaaaa	cgtccaatac	gtagatggaa	360
38	acgatctcaa	ttcatccatc	gacggcggaa	ctgggttcaa	400
39	ttttatcaac	gtagatcgca	taaacatcaa	tacgatccgc	440
40	agtgggtggc	gccggaatat	ggcaccagga	aatcttaaca	480
41	ctgtttccca	aggtatctct	ttgaatgcaa	attgtcagac	520
42	tgtaattata	ggcaacgcag	ttaccacaaa	ctggtgaagt	560
43	cacggttttt	atagccaagc	tcaggacatt	ttggttaatg	600
44	gtctgatac	acgtgataat	ggcggaaagg	ggtacgttgc	640
45	agagggttca	gcagggtcat	ctctcctaaa	tggggccgtt	680
46	ttcagagata	atgtagcagg	gaattatttt	acaggaggga	720
47	caagcgtaaa	ccatctcgcg	aacttccaac	ttcataaactc	760
48	tagcaccggg	gggaaaactt	ttgtggccaa	tgtcaccaca	800
49	aatgggtctg	cataacggtc	cttgccattt	taactataaa	840

delete Do not insert alphabetical headings, the CRF software will insert them.
 Does Not Comply Corrected Dickette Needed <150> US 60/533,016 <151> 2003-09-15

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Input Set : A:\10733691.txt

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50 tgagctattc ccgcgcatta agagtagaca cgggaaatca 880
51 gtatggctcc gagacatatt acagttatcc taccagctaa 920
52 gtaccgaggc ggaagtcttc gagttacgaa gaatatcgtt 960
53 cgaatgcttt tgaagggaag tcagaattat ggtgaacagt 1000
54 gtcaagttag attggcagta cgtgccgata cctacgatat 1040
55 tggggaggag ttctgtgatc ttatcgataa tgggtgtagag 1080
56 gttcgggaaa tatcattcaa agaagttcct ccagaagatg 1120
57 ttaacaatgc taactatttc caaggtagaa atatcgacct 1160
58 acagtcgaga acctattggc taatggagga tggccaaaac 1200
59 aactgtgccg atagtgcctt ttggctagtt gtatcctact 1240
60 ctgtagagta tcctattgcc ccgataaggc cgacactgat 1280
61 atttgccacc gatttcattc aaaggtacgt acctgatatt 1320
62 atttgccacc cacggcccgg tgagggggat gctgaggctc 1360
63 ttgcgttctt acgacaatca gacggcgtac tagctacaac 1400
64 accacacacg cggtcggatg cgatttcata cgctggctta 1440
65 cctgcgtcca aagtttatct tgctccgatg gagtttgacc 1480
66 cgacgttttt ggatcgttac cggtcagtg taaaggttta 1520
67 ggaaccctat ttcttttggc caaccaaccc aaatgctcac 1560
68 aaaaaccatg caaaagcgtt tcaagcgcta gacctatatt 1600
69 acggcaaaact aaagggtaa ataaagacaa agatagtcgg 1640
70 tgtgagtagt gtgcggatgg acccatccca tcgatggcag 1680
71 gccaaagtacg aaaataaggc ttatgtgaaa tctgtacggg 1720
72 aaattgttgc gggctctcgc aacctgaaaa gcaatgttga 1760
73 gttcgttggg gaggttgcgg acaaggagta tgcggagctt 1800
74 cttgcttcag cttgtttcct ttggcatcca actttggcag 1840
75 acaacggaac ttttgcgtcg gtcgaagcgg catatatggg 1880
76 atgtccaacg ctttcaaacg actaccgcga gatgcggtat 1920
77 atttctaacc gtttcgaaat tcccatgcag tattttaacg 1960
78 caaggtctgt gaaggaaatg gcatcagcgc ttaagcaaat 2000
79 ggaggagacg ccaatagatg taggtttatt gccaaagtcga 2040
80 gaaaccctat ctctgcattc gtgggaagct cacgccttcg 2080
81 aatactggga tgtgatcgtg agggcagcgg catgaataag 2120
82 ctgcgcgtgt ttatcggtc taaccagggc caattagatc 2160
83 catatcaggg tatttctcgc ttaattgcat tcgtgatcaa 2200
84 gggggccttg aaccagggtg gcggtgtaac aattgcttgc 2240
85 cccggtcgtg taaaggacga tgtacgtgtt cttttggaag 2280
86 atgctgatat ccacttgaa gcggtcaaaa ttatcgcgac 2320
87 gaatggtcag cctccattgg ctctgttatg gaagttgaga 2360
88 gataaattcc gtaagagacg gacgagtaaa cgaaaacgtc 2400
89 tctggctgga gcgctatggs aaaaatgttg caaattttgt 2440
90 tgcagaatgg ctttctttgc gctcgtattg ggggattttt 2480
91 ttgggggctg ctgcaattgc tgtagtgact attctacttg 2520
92 ccgtaccaat tgctatagcc ttcaccgctc ttatcggctc 2560
93 tctatttgct cgtcggctta ttagacgtgt tatcaggtca 2600
94 aagcttggtt tgttttttca caaaaatgcc aatcaattca 2640
95 acaaattaat gtcactctgat gaaaccatcg accggatgag 2680

```

OK
E--> 98 <210> SEQ ID NO: SEQ ID NO 2
99 <211> LENGTH: LENGTH: 410

delete

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TIME: 11:25:40

Input Set : A:\10733691.txt

Output Set: N:\CRF4\12302003\J733691.raw

```

E--> 100 <212> TYPE: TYPE: PRT
      101 <213> ORGANISM: ORGANISM: Brucella melitensis
E--> 102 <400> SEQUENCE: SEQUENCE 2
      103 Met Ala Pro Arg His Ile Thr Val Ile Leu
E--> 104      5      10 5      10
      105 Pro Ala Lys Tyr Arg Gly Gly Ser Leu Arg
E--> 106      15 15      20 20
      107 Val Thr Lys Asn Ile Val Arg Met Leu Leu
E--> 108      25      30
      109 Lys Gly Ser Gln Asn Tyr Gly Glu Gln Cys
E--> 110      35      40
      111 Gln Val Arg Leu Ala Val Arg Ala Asp Thr
E--> 112      45      50
      113 Tyr Asp Ile Gly Glu Glu Phe Arg Asp Leu
E--> 114      55      60
      116 Ile Asp Asn Gly Val Glu Val Arg Glu Ile
E--> 117      65      70
      118 Ser Phe Lys Glu Val Pro Pro Glu Asp Val
E--> 119      75      80
      120 Asn Asn Ala Asn Tyr Phe Gln Gly Arg Asn
E--> 121      85      90
      122 Ile Asp Leu Gln Ser Arg Thr Tyr Trp Leu
E--> 123      95      100
      124 Met Glu Asp Gly Gln Asn Asn Cys Ala Asp
E--> 125      105      110
      126 Ser Asp Leu Trp Leu Val Val Ser Tyr Ser
E--> 127      115      120
      128 Val Glu Tyr Pro Ile Ala Pro Ile Arg Pro
E--> 129      125      130
      130 Thr Leu Ile Phe Ala Thr Asp Phe Ile Gln
E--> 131      135      140
      132 Arg Tyr Val Pro Asp Ile Ile Trp Pro Pro
E--> 133      145      150
      134 Arg Pro Gly Glu Gly Asp Ala Glu Ala Leu
E--> 135      155      160
      136 Ala Phe Leu Arg Gln Ser Asp Gly Val Leu
E--> 137      165      170
      138 Ala Thr Thr Pro His Thr Arg Leu Asp Ala
E--> 139      175      180
      140 Ile Ser Tyr Ala Gly Leu Pro Ala Ser Lys
E--> 141      185      190
      142 Val Tyr Leu Ala Pro Met Glu Phe Asp Pro
E--> 143      195      200
      144 Thr Phe Leu Asp Arg Tyr Arg Ser Val Ser
E--> 145      205      210
      146 Lys Val Lys Glu Pro Tyr Phe Leu Trp Pro
E--> 147      215      220
      148 Thr Asn Pro Asn Ala His Lys Asn His Ala
E--> 149      225      230

```

*misaligned
amino acid numbers
(see item 3 on Error
summary sheet)*

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TIME: 11:25:40

Input Set : A:\10733691.txt

Output Set: N:\CRF4\12302003\J733691.raw

150 Lys Ala Phe Gln Ala Leu Asp Leu Tyr Tyr
E--> 151 235 240
152 Gly Lys Leu Lys Gly Lys Ile Lys Thr Lys
E--> 153 245 250
154 Ile Val Gly Val Ser Ser Val Arg Met Asp
E--> 155 255 260
156 Pro Ser His Arg Trp Gln Ala Lys Tyr Glu
E--> 157 265 270
158 Asn Lys Ala Tyr Val Lys Ser Val Arg Glu
E--> 159 275 280
160 Ile Val Ala Gly Leu Asp Asn Leu Lys Ser
E--> 161 285 290
162 Asn Val Glu Phe Ala Gly Glu Val Ala Asp
E--> 163 295 300
164 Lys Glu Tyr Ala Glu Leu Leu Ala Ser Ala
E--> 165 305 310
166 Cys Phe Leu Trp His Pro Thr Leu Ala Asp
E--> 167 315 320
168 Asn Gly Thr Phe Ala Ala Val Glu Ala Ala
E--> 169 325 330
170 Tyr Met Gly Cys Pro Thr Leu Ser Asn Asp
E--> 171 335 340
172 Tyr Pro Gln Met Arg Tyr Ile Ser Asn Arg
E--> 173 345 350
174 Phe Glu Ile Pro Met Gln Tyr Phe Asn Ala
E--> 175 355 360
176 Arg Ser Val Lys Glu Met Ala Ser Ala Leu
E--> 177 365 370
178 Lys Gln Met Glu Glu Thr Pro Ile Asp Val
E--> 179 375 380
180 Gly Leu Leu Pro Ser Arg glu Thr Leu Ser
E--> 181 385 390
182 Leu His Ser Trp Glu Ala His Ala Ser Glu
E--> 183 395 400
184 Tyr Trp Asp Val Ile Val Arg Ala Ala Ala
E--> 185 405 410

*same**enw*

VERIFICATION SUMMARY

DATE: 12/30/2003

PATENT APPLICATION: US/10/733,691

TIME: 11:25:41

Input Set : A:\10733691.txt

Output Set: N:\CRF4\12302003\J733691.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:
L:18 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:
L:23 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:25 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:27 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:28 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:96 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:2693 SEQ:0
L:98 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:100 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:102 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:104 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
M:332 Repeated in SeqNo=0
L:185 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:410 SEQ:0